The nucleotide sequences of the 5S rRNAs from the purple bacteria *Ectothiorhodospira halophila* and *Ectothiorhodospira vacuolata*

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Submitted December 1, 1986

5 S rRNA preparations obtained from *Ectothiorhodospira halophila* BN 9624 (strain collection of the department of Microbiology, University of Bonn, FRG) and from *Ectothiorhodospira vacuolata* ATCC 43036 were 3'-terminally labeled by ligation to [5'-^{32}P]pCp. Components of different chain length resolved by gel electrophoresis were individually sequenced by the partial chemical degradation method (1). The sequences in the neighbourhood of the 5'-termini were determined by partial nuclease degradation after extension of the 5'-termini by ligation to $(Ap)_4A$ (2). The following sequences were derived.

E. halophila pUGCCUGGCGACCAUAGCGAGCGGGAACCACCCGAUCCGAUGCCGAACUCGGCAGUG
E. vacuolata pUACCUGGCGGCCAUGGCGAACCGGAACCACCCGAUCCCAUCUCGAACUCGGAAGUG

A B C C

AAACCGCUCAGCGCCGAUGGUAGUGCGACCACGCUGUCGUGCGAGAGUAGGUCAUCGCCAGGCCc
AAACGGUUCAGCGCCGAUGAUAGUGUGGGG-CCUCCCCAUGUGAAAGUAGGUCACUGCCAGGCAc

B' D E E' D' A'

Boxes on the alignment enclose double-stranded areas labeled according to a previously documented (3) 5 S RNA secondary structure model. Residues printed in lower case are present in submolar amounts. Three components present in *E. vacuolata* 5 S RNA have the following termini :

pUAC ---------- AC (chain length 120)
pUAC ---------- A (chain length 119)
pC ---------- AC (chain length 118)

The bacteria belonging to the genus *Ectothiorhodospira* were shown (4) by 16 S rRNA oligonucleotide cataloguing to belong to the group of purple bacteria subdivision γ as defined in (5). The same relationship was found (unpublished) when the Ectothiorhodospira 5 S RNA sequences were clustered with sequences from 121 bacterial species according to the method described in (6).

References

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